



- 1 -

SEQUENCE LISTING

<110> Evans, Glen A.

<120> Non-Immunoglobulin Binding Polypeptides

<130> 66663-026

<140> US 10/611,655

<141> 2003-06-30

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 162

<212> PRT

<213> Homo sapiens

<400> 1

Met Asn Leu Ala Ile Ser Ile Ala Leu Leu Leu Thr Val Leu Gln Val
1 5 10 15
Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln
20 25 30
Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Pro Ile
35 40 45
Gln Tyr Glu Glu Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe
50 55 60
Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe
65 70 75 80
Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser
85 90 95
Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser
100 105 110
Pro Pro Ile Leu Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu
115 120 125
Val Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser Trp Leu
130 135 140
Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr Asp Phe Met
145 150 155 160
Ser Leu

<210> 2

<211> 124

<212> PRT

<213> Homo sapiens

<400> 2

Gln Leu Gln Gln Ser Gly Glu Ala Leu Val Lys Pro Gly Ala Ser Val

1	5	10	15
Arg Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Pro Asn Tyr Trp Met			
20	25	30	
His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Thr			
35	40	45	
Ile Asp Pro Ala Asp Ser Tyr Thr Ser Tyr Asn Gln Asn Phe Lys Asp			
50	55	60	
Lys Ala Thr Leu Thr Val Lys Pro Ser Ser Thr Ala Tyr Met Gln Leu			
65	70	75	80
Ser Ser Leu Thr Phe Gly Asp Ser Ala Val Tyr Phe Cys Ala Arg Glu			
85	90	95	
Ser Tyr Tyr Tyr Arg Tyr Phe Asp Tyr Trp Gly His Gly Thr Thr			
100	105	110	
Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu			
115	120		

<210> 3

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus peptide

<400> 3

Gln Leu Ser Leu Lys Leu Cys Lys Ser Ser Phe Arg Gly Thr Ile Asp			
1	5	10	15
Asn Phe Lys Asp Ala Thr Thr Ser Ile Ser Ser Glu Gly Ile Trp Leu			
20	25	30	
Ser Leu Ser Thr Leu			
35			

<210> 4

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> ThyOx non-immunoglobulin binding polypeptide

<400> 4

Gln Val Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val			
1	5	10	15
Asp Gln Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser			
20	25	30	
Asn Tyr Trp Met His Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val			
35	40	45	
Leu Phe Gly Thr Ile Asp Pro Ala Asp Ser Tyr Thr Ser Tyr Asn Gln			
50	55	60	
Asn Phe Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly			
65	70	75	80
His Ser Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys			
85	90	95	

Leu Val Lys Cys Glu Gly Val Tyr Tyr Arg Tyr Tyr Phe Asp Tyr
100 105 110

<210> 5
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<223> carrier encoding erythropoietin

<221> CDS
<222> (21) ... (1022)

<400> 5
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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp
1 5 10

ctg ctg ctg agc ctg agc ctg ccc ctg ggc ctg ccc gtg ctg ggc 101
Leu Leu Leu Ser Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
15 20 25

gcc ccc ccc cggtt ctg atc tgc gac agc cggtt ctg gag cggtt cac ctg 149
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg His Leu
30 35 40

ctg gag gcc aag gag gcc gag agc atc acc acc ggc tgc gtg gag gac 197
Leu Glu Ala Lys Glu Ala Glu Ser Ile Thr Thr Gly Cys Val Glu Asp
45 50 55

tgc agc ctg aac gag aac atc acc acc gtg ccc gac agc aag gtg aac ttc 245
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Ser Lys Val Asn Phe
60 65 70 75

tac gcc tgg aag cggtt atg gag gtg ggc cag cag gcc gtg gag gtg tgg 293
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
80 85 90

cag ggc ctg gcc ctg ctg agc gag gcc gtg ctg cggtt ggc cag gcc ctg 341
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
95 100 105

ctg gtg atc agc agc cag ccc tgg gag ccc ctg cag ctg cac gtg gac 389
Leu Val Ile Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
110 115 120

aag gcc gtg agc ggc ctg cggtt agc ctg acc acc ctg ctg cggtt gcc ctg 437
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
125 130 135

ggc gcc cag aag gag gcc atc agc ccc ccc gac gcc ggc agc ggc ggc 485
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala

140	145	150	155	
ccc ctg cgg acc atc acc gcc gac acc ttc cgg aag ctg ttc cgg gtg Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val				533
160	165		170	
tac ccc aac ttc ctg cgg ggc aag ctg aag ttc tac acc ggc gag gcc Tyr Pro Asn Phe Leu Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala				581
175	180		185	
tgc cgg ggc ggc ggc ggc agc ggc ggc ggc gag ttc ggc ggc Cys Arg Gly Gly Gly Ser Gly Gly Gly Glu Phe Gly Gly				629
190	195		200	
ggc ggc agc cag aag gtg acc agc ctg acc gcc tgc ctg gtg gac cag Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln				677
205	210		215	
agc ctg cgg ctg gac tgc cgg cac gag aac acc agc agc agc ccc atc Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile				725
220	225		230	
235				
cag tac gag ttc agc ctg acc cgg gag acc aag aac cac gtg ctg ttc Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe				773
240	245		250	
ggc acc gtg ggc gtg ccc gag cac acc tac cgg agc cgg acc aac ttc Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe				821
255	260		265	
acc agc aag tac cac atg aag gtg ctg tac ctg agc gcc ttc acc agc Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser				869
270	275		280	
aag gac gag ggc acc tac acc tgc gcc ctg cac cac agc ggc cac agc Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser				917
285	290		295	
ccc ccc atc agc agc cag aac gtg acc gtg ctg cgg gac aag ctg gtg Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val				965
300	305		310	
315				
aag tgc gag ggc atc agc ctg ctg gcc cag aac acc agc cac cac cac Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His				1013
320	325		330	
cac cac cac tgatgataag atcggatcct aggcttcc His His His				1050

<212> PRT

<213> Artificial Sequence

<220>

<223> chimeric ThyOx carrier polypeptide containing
erythropoietin

<400> 6

Met	Gly	Val	His	Glu	Cys	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Leu	Ser	Leu
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Leu	Ser	Leu	Pro	Leu	Gly	Leu	Pro	Val	Leu	Gly	Ala	Pro	Pro	Arg	Leu
						20			25					30	
Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	His	Leu	Leu	Glu	Ala	Lys	Glu
						35			40			45			
Ala	Glu	Ser	Ile	Thr	Thr	Gly	Val	Glu	Asp	Cys	Ser	Leu	Asn	Glu	
						50			55			60			
Asn	Ile	Thr	Val	Pro	Asp	Ser	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg
						65			70		75			80	
Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu
						85			90			95			
Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Ile	Ser	Ser
						100			105			110			
Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly
						115			120			125			
Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu
						130			135			140			
Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile
						145			150		155			160	
Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Pro	Asn	Phe	Leu
						165			170			175			
Arg	Gly	Lys	Leu	Lys	Phe	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Gly	Gly	Gly
						180			185			190			
Gly	Gly	Ser	Gly	Gly	Gly	Glu	Phe	Gly	Gly	Gly	Ser	Gln	Lys		
						195			200			205			
Val	Thr	Ser	Leu	Thr	Ala	Cys	Leu	Val	Asp	Gln	Ser	Leu	Arg	Leu	Asp
						210			215			220			
Cys	Arg	His	Glu	Asn	Thr	Ser	Ser	Ser	Pro	Ile	Gln	Tyr	Glu	Phe	Ser
						225			230		235			240	
Leu	Thr	Arg	Glu	Thr	Lys	Lys	His	Val	Leu	Phe	Gly	Thr	Val	Gly	Val
						245			250			255			
Pro	Glu	His	Thr	Tyr	Arg	Ser	Arg	Thr	Asn	Phe	Thr	Ser	Lys	Tyr	His
						260			265			270			
Met	Lys	Val	Leu	Tyr	Leu	Ser	Ala	Phe	Thr	Ser	Lys	Asp	Glu	Gly	Thr
						275			280			285			
Tyr	Thr	Cys	Ala	Leu	His	His	Ser	Gly	His	Ser	Pro	Pro	Ile	Ser	Ser
						290			295			300			
Gln	Asn	Val	Thr	Val	Leu	Arg	Asp	Lys	Leu	Val	Lys	Cys	Glu	Gly	Ile
						305			310		315			320	
Ser	Leu	Leu	Ala	Gln	Asn	Thr	Ser	His							
						325			330						

<210> 7

<211> 1050

<212> DNA

<213> Artificial Sequence

<220>

<223> SuperEpo

<221> CDS

<222> (21) . . . (1022)

<400> 7

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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp
1 5 10

ctg ctg ctg agc ctg ctg agc ctg ccc ctg ggc ctg ccc gtg ctg ggc 101
 Leu Leu Leu Ser Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
15 20 25

gcc ccc ccc cg^g ctg atc tgc gac agc cg^g gtg ctg gag cg^g cac ctg 149
 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg His Leu
 30 35 40

ctg gag gcc aag gag gcc gag agc atc acc acc ggc tgc gtg gag gac 197
 Leu Glu Ala Lys Glu Ala Glu Ser Ile Thr Thr Gly Cys Val Glu Asp
 45 50 55

tgc agc ctg aac gag aac atc acc gtg ccc gac agc aag gtg aac ttc 245
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Ser Lys Val Asn Phe
 60 65 70 75

tac gcc tgg aag cg^g atg gag gtg ggc cag cag gcc gtg gag gtg tgg 293
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
80 85 90

cag ggc ctg gcc ctg ctg agc gag gcc gtg ctg cgg ggc cag gcc ctg 341
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 95 100 105

ctg gtg atc agc agc cag ccc tgg gag ccc ctg cag ctg cac gtg gac 389
 Leu Val Ile Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 110 115 120

aag gcc gtg agc ggc ctg cg	agc ctg acc acc ctg ctg cg	gg gcc ctg	437
Lys Ala Val Ser Gly Leu Arg	Ser Leu Thr Thr Leu Leu Arg	Ala Leu	
125	130	135	

ggc gcc cag aag gag gcc atc agc ccc ccc gac gcc gcc agc gcc gcc 485
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
140 145 150 155

ccc ctg cgg acc atc acc gcc gac acc ttc cgg aag ctg ttc cgg gtg
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 160 165 170

tac ccc aac ttc ctg cg ^g ggc aag ctg aag ttc tac acc ggc gag gcc Tyr Pro Asn Phe Leu Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala 175 180 185	581
tgc cg ^g ggc ggc ggc gg ^c agc gg ^c ggc gg ^c gag ttc ggc ggc Cys Arg Gly Gly Gly Ser Gly Gly Glu Phe Gly Gly 190 195 200	629
ggc ggc agc cag aag gtg acc agc ctg acc gcc tgc ctg gtg gac cag Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln 205 210 215	677
agc ctg cg ^g ctg gac tgc cg ^g cac gag aac acc agc agc ccc atc Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile 220 225 230 235	725
cag tac gag ttc agc ctg acc cg ^g gag acc aag aag cac gtg ctg ttc Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe 240 245 250	773
ggc acc gtg ggc gtg ccc gag cac acc tac cg ^g agc cg ^g acc aac ttc Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe 255 260 265	821
acc agc aag tac cac atg aag gtg ctg tac ctg agc gcc ttc acc agc Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser 270 275 280	869
aag gac gag ggc acc tac acc tgc gcc ctg cac cac agc ggc cac agc Lys Asp Glu Gly Thr Tyr Cys Ala Leu His His Ser Gly His Ser 285 290 295	917
ccc ccc atc agc agc cag aac gtg acc gtg ctg cg ^g gac aag ctg gtg Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val 300 305 310 315	965
aag tgc gag ggc atc agc ctg ctg gcc cag aac acc agc cac cac cac Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His 320 325 330	1013
cac cac cac tgatgataag atcggtatcct aggcttcc His His His	1050

<210> 8
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> SuperEpo

<400> 8

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15
Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30
Ile Cys Asp Ser Arg Val Leu Glu Arg His Leu Leu Glu Ala Lys Glu
35 40 45
Ala Glu Ser Ile Thr Thr Gly Cys Val Glu Asp Cys Ser Leu Asn Glu
50 55 60
Asn Ile Thr Val Pro Asp Ser Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Ile Ser Ser
100 105 110
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140
Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Pro Asn Phe Leu
165 170 175
Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala Cys Arg Gly Gly Gly
180 185 190
Gly Gly Ser Gly Gly Gly Glu Phe Gly Gly Gly Ser Gln Lys
195 200 205
Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln Ser Leu Arg Leu Asp
210 215 220
Cys Arg His Glu Asn Thr Ser Ser Pro Ile Gln Tyr Glu Phe Ser
225 230 235 240
Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe Gly Thr Val Gly Val
245 250 255
Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe Thr Ser Lys Tyr His
260 265 270
Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser Lys Asp Glu Gly Thr
275 280 285
Tyr Thr Cys Ala Leu His His Ser Gly His Ser Pro Pro Ile Ser Ser
290 295 300
Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val Lys Cys Glu Gly Ile
305 310 315 320
Ser Leu Leu Ala Gln Asn Thr Ser His His His His His His His
325 330

<210> 9

<211> 600

<212> DNA

<213> Artificial Sequence

<220>

<223> carrier encoding glucagon-like peptide 1

<221> CDS

<222> (29)...(556)

<400> 9

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tct gac gtt tct tac ctg gaa ggt cag gcg aaa gag ttc atc
Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile
10 15 20

gcg tgg ctg gtt aaa ggt cgt ggt ggt ggt tct ggt ggt ggt
Ala Trp Leu Val Lys Gly Arg Gly Gly Ser Gly Gly Gly
25 30 35 40

ggt gag ttc ggt ggt tct cag aaa gtt acc tct ctg acc gcg
Gly Glu Phe Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala
45 50 55

tgc ctg gtt gac cag tct ctg cgt ctg gac tgc cgt cac gaa aac acc
Cys Leu Val Asp Gln Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr
60 65 70

tct tct tct ccg atc cag tac gag ttc tct ctg acc cgt gaa acc aaa
Ser Ser Ser Pro Ile Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys
75 80 85

aaa cac gtt ctg ttc ggt acc gtt ggt ccg gaa cac acc tac cgt
Lys His Val Leu Phe Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg
90 95 100

tct cgt acc aac ttc acc tct aaa tac cac atg aaa gtt ctg tac ctg
Ser Arg Thr Asn Phe Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu
105 110 115 120

tct gcg ttc acc tct aaa gac gaa ggt acc tac acc tgc gcg ctg cac
Ser Ala Phe Thr Ser Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His
125 130 135

cac tct ggt cac tct ccg atc tct tct cag aac gtt acc gtt ctg
His Ser Gly His Ser Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu
140 145 150

cgt gac aaa ctg gtt aaa tgc gaa ggt atc tct ctg ctg gcg cag aac
Arg Asp Lys Leu Val Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn
155 160 165

acc tct cac cac cac cac tgataatgag atcttgaggc cgatatcgct
Thr Ser His His His His His
170 175

taagatcccc gcaa 600

<210> 10
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> chimeric ThyOx carrier polypeptide containing
glucagon-like peptide 1

<400> 10
Met His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu
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20 25 30
Gly Gly Gly Ser Gly Gly Glu Phe Gly Gly Gly Ser
35 40 45
Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln Ser Leu Arg
50 55 60
Leu Asp Cys Arg His Glu Asn Thr Ser Ser Pro Ile Gln Tyr Glu
65 70 75 80
Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe Gly Thr Val
85 90 95
Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe Thr Ser Lys
100 105 110
Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser Lys Asp Glu
115 120 125
Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser Pro Pro Ile
130 135 140
Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val Lys Cys Glu
145 150 155 160
Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His His His
165 170 175

<210> 11
<211> 4000
<212> DNA
<213> Artificial Sequence

<220>
<223> vector pEgea M3

<400> 11
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ctttccattt acgtcaatgg gtggagtatt tacgttaaac tgcccacttg gcagtacatc 180
aagtgtatca tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgct 240
ggcattatgc ccagtacatg accttatggg acttcctac ttggcagtagc atctacgtat 300
tagtcatcgc tattaccatg gtgatgcgtt tttggcagta catcaatggg cgtggatagc 360
ggtttactc acggggattt ccaagtctcc acccattga cgtcaatggg agtttgttt 420
ggcaccaaaa tcaacgggac tttccaaaat gtcgtaacaa ctccgcccc ttgacgcaaa 480
tgggcgttag gcgtgtacgg tgggaggtct atataagcag agctctctgg ctaactagaa 540
tcgaaattaa tacgactcac tatagggaga cccaaagctgg ctacgcgttta aacttaagct 600

tggtaaccgag	ctcgatcca	ctctaggggg	tatccccacg	cgcctgttag	cggcgcatta	660
agcgcggcgg	gtgtgggtt	tacgcgcagc	gtgaccgcta	cacttgcacag	cgccttagcg	720
cccgctcctt	tcgcttctt	cccttcctt	ctcgccacgt	tcgcccgtt	tccccgtcaa	780
gctctaaatc	gggggctccc	tttagggttc	cgatttagtg	cttacggca	cctcgacccc	840
aaaaaaactt	attagggta	tggttacagt	agtggccat	cgcctgata	gacggttttt	900
cgcctttga	cgttggagtc	cacgttctt	aatagtggac	tcttggcca	aactggaaaca	960
acactcaacc	ctatctcggt	ctattcttt	gatttataag	ggatttgcc	gatttcggcc	1020
tattggtaa	aaaatgagct	gatthaacaa	aaatthaacg	cgaattaatt	ctgtggaaatg	1080
tgtgtcagtt	agggtgtgga	aagtccccag	gctccccagc	aggcagaagt	atgcaaaagca	1140
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gtatgaaag	catgcacatc	aatttagtcag	caaccatagt	cccgccccca	actccgcccc	1260
tcccgcccc	aactccgccc	agttccgccc	attctccgccc	ccatggctga	ctaatttttt	1320
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gcttttttgg	aggccttaggc	ttttgcaaaaa	agctcgagga	tcgttgcga	tgattgaaca	1440
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ggcacacaacag	acaatccgct	gctctgtatgc	cgcgtgttgc	cggctgtcag	cgcaggggcg	1560
cccggttctt	tttgtaaga	ccgacctgtc	cggtgcctg	aatgaactgc	aggacgaggc	1620
agcgcggcta	tcgtgctgg	ccacgacggg	cgttccttgc	gcagctgtgc	tcgacgttgt	1680
cactgaagcg	ggaagggact	ggctgtatt	ggcgaagtgc	ccggggcagg	atctcctgtc	1740
atctcacctt	gctcctgccc	agaaagtatc	catcatggct	gatgcaatgc	ggcggctgca	1800
tacgcttgc	ccggctacct	gcccattcga	ccaccaagcg	aaacatcgca	tcgagcgagc	1860
acgtactcgg	atggaagccg	gtcttgcga	tcaggatgt	ctggacgaag	agcatcaggg	1920
gctcgcgc	gccgaactgt	tcgcccaggt	caaggcgcgc	atgcccgcgc	gcfaggatct	1980
cgtcgtgacc	catggcgatg	cctgcttgc	aatatcatg	gtggaaaatg	gccgcttttc	2040
tggattcatc	gactgtggcc	ggctgggtgt	ggcggaccgc	tatcaggaca	tagcgttgc	2100
tacccgtat	attgctgaag	agcttggccg	cgaatggct	gaccgcttcc	tcgtgttta	2160
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